

Human 23565

Carboxypeptidase Activation Peptide Domain

Zinc Carboxypeptidase Domain

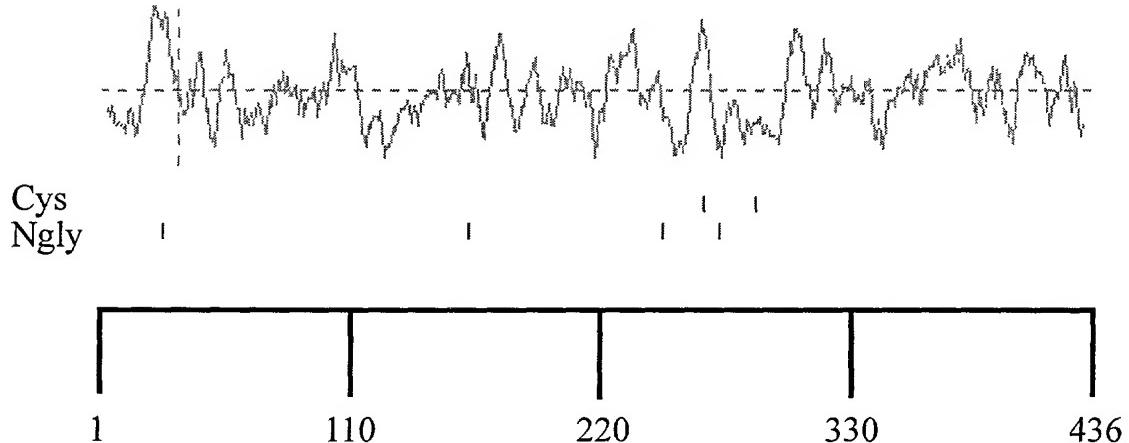


Fig. 1

Zn_carbOpept: domain 1 of 1, from 139 to 419: score 413.7, E = 1.7e-120

* ->Yhnleeiyaw1D11vsnfPdLlvskvsiGksyeGRdlkvLK1sdnpat
 Yh+leeiy+w+D+ v ++ d+vsk++iG+s+e+ + VLK+s++
 YHTLEEIIYSWIDNFMEMHSDIVSKIQIGNSFENQSILVLKFSTG--- 182

genePevfavagWIHAREwvtsAt11w11kelvanYgsDktitk11dg1d
 g++ P+++++g iH+REw+t At w+++++v++Yg D t++l+ +d
 Fbh23565f1 183 GSRHPAIWIDTG- IHSREWITHTGIWTANKIVSDYGKDRVLTIDLNAMD 231

1fyilpvfNpDGyayssittdsYRmWRKtRsponagsfcvgtDpNRNWyaqw
 ++i v+NpDG+a+++ + R+WRK+ s ++g fc+G+D+NRNW +++
 Fbh23565f1 232 -IFILELVTNPDGFIAFTHSMN--RLWRKNKSIRPGIIFCIGVDLNRNWKSGF 278 -

ggmgassysPcSetYeGtapfSepEtkaVEDfirsw1ggGkqnIkayItf
 gg g +s +PcSetY+G+ p Se E++a+++fi ++ n ka+I++
 Fbh23565f1 279 GGNGSNS-NPCSETYHGPPSPQSESEVAATVNFIITAIG---- NFKALISI 322

HsYSQ111YPYgydyn1npand1dels1kiaadalsarhgtyyt1glp
 HsYSQ+1+YPYg+ + + + +1 +1 + Kr a+ a1 hg Y g +
 Fbh23565f1 323 HSYSQMLMYPYGRILLEPVSNQRELYDLA--KDAVEAALYKVHIGIEYIFG-S 369

gsstIYpasAGGsdDwaydvgiikyaftfElrpdtgsyGnPcf11PeeqI
 +s+t+Y+as G + Dwayd g ikyaf fElr dtg YG F11P+-qI
 Fbh23565f1 370 ISTTLYVAS-GITVDWAYDSG- IKYAFSFELR-DTGQYG---FLLPATQI 413

iptgsee<-* (SEQ ID NO: 4)
 ipt++ e
 Fbh23565f1 414 IPTAQ-E 419

Fig. 2A

zn_carb: domain 1 of 1, from 139 to 419: score 401.8, E = 6.7e-117

*	->	Yhsyeeinaw1ddLarnyPdltsvs1is1GksyeGRpikv1k1	...	
Yh+	+eei+	w+d+	+++ d+	Vs i+ig+s+e++ i+v1k++++
Fbh23565f1	139	YHTLEEIIYSWIDNFVMEHSDI - VSKIQIGNSFENQSILVLKFstgg	183	
..	kpavfidagihAREWiapatalylinqltneteyskdpddegsvtk1			
++ pa++id	giH REWi+	at	+++n++++ Y+kd ++ t++	
Fbh23565f1	184	srHPAIWIDTGIHSREWITHATGIWTANKIVSD-- YGKD-RV---LTDI	226	
Ldk1dwyi vPvmNPDGyeythtstdR1WRKnRspngasgsqgtwynCyGv				
L+ +d+i v+NPDG++th+ ++R1WRKn s	+	C+GV		
Fbh23565f1	227	LNAMDIFIELVTNPDGFATHS-MNRLWRKNKSIRPG-----IF-CIGV	268	
D1NRRNfdfhnWgeigGss1pCsetYagsspfSeWepektakk1dfilsne				
D1NRRN+ ++ +g+ GS+s+pCsetY+G+sp+S E E+ a+ +fi+ +				
Fbh23565f1	269	D1NRRNWKG-FGGN-GSNSNPCSETYHGFPSPQS- -ESEVAIAIVNFI	313	
TAH- igkgrikayi1HsysqllyPyGytnatvppngedlhkevakaakraig				
g+ka is+Hsysq+1+yPYG + ++n++1 ++ak a++a+				
Fbh23565f1	314	--GNFKALISIHSYSQMLMYPYGRILL-EPVSNQRELY-DLAKDAVEA	358	
LY 358				
dyyfgct1YtpGssadpd1ditlypasGgsdDwaygt1kgvkyssytIEL				
+++ G Y G s++ t1Y asG++ Dway+ + +ky++ +EL				
Fbh23565f1	359	KVH- -GIEYIFG-SIST----TLYVASGITVDWAYDSG-- IKYAFSFEL	398	
rdtgddagrygF1LppscvkpvrmegiqiptgeE<-* (SEQ ID NO: 5)				
rdt g+ygF1Lp+ qipt+ E				
Fbh23565f1	399	RDT----GQYGFLLPA-----TQIIPTAQE	419	

Fig. 2B

Propep_M14: domain 1 of 1, from 41 to 118: score 100.3, E = 3.8e-26

<pre>* ->QV1rvkvadedQvk11kdlenteheleldFWkpdsatpiKpgstvDfr QV1rv + de+Q++11 dIe ++ DFW++ P++P +vD r QVLRLAKDEKQLSLLGDLEGKPKQKVDFWRG----PARPSLPPVDMR 83</pre>	<pre>VpaediqavksfLeqsgihYevvlieDVqeIIeeqf <- * (SEQ ID NO: 6) Vp++++++k++ Le++g+ Y++I D q+ll+e+++ VPFSELKDIIKAYLESHGGLAYSIMIKDIQVLLDEER 118</pre>
--	--

Fbh23565f1 41

Fbh23565f1 84

Fig. 3